

Best Local Similarity: 85.19% Mismatches: 0
Query Match: 81.68% Indels: 20
DB: 9 Gaps: 1

US-10-005-907-2 (1-135) x AK126682 (1-4032)

QY 1 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys 20
DB 377 ATGGGAATATCTCTCGGAAACTC----- 403

QY 21 LysGlyAsnProLysGluGlyArgGlnGluMetThrThrPheGluArgLysLeu 40
DB 404 -----AGGAGGAATGACTCACTTTGAAGAACTT 436

QY 41 GlnPheArgGluLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGlu 60
DB 437 CAGCAACAGATAGAAAGCCAGAGTTTTCATCTCTTAATACGAAACGAGAAAT 496

QY 61 GlySerLysSerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer 80
DB 497 GGCAGTCTCTGGAAGAGTGCTACACTGTCTAATATCATCTCCCATCCAGAGATCC 556

QY 81 SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
DB 557 TCCCTGAGTCATGATGATGCTATGAGACATGCTCTCCCTCAGAGAAAGTGAGA 616

QY 101 GlnPheArgGluLysSerGlnGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro 120
DB 617 CAGTTTAGAAGAGTGAGAGACAGATATGCCCTTCTTAGAGCTTCTGTAGTAGGCTT 676

QY 121 CysSerCysThrHisGlnHisAspTyrGluValValPheProHis 135
DB 677 TGTCTCTGACCCATGAGCATGATTATGAGTTGTTGTTTCCACAC 721

RESULT 6
AK124520 4136 bp mRNA linear PRI 09-SEP-2003
LOCUS Homo sapiens cDNA FLJ45292 f1a, clone BRACE3002390.
DEFINITION AK124520
ACCESSION AK124520
VERSION AK124520.1 GI:34530324
KEYWORDS oligo capping f1a (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuma, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yanashita, H., Matsumoto, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kawahori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagata, K., Masuno, Y., Nagai, K. and Inogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 4136)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI); (supported by Japan
Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
1. 4136

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRACE3002390"
/tissue_type="cerebellum"
/clone_lib="BRACE3"
/notes="cloning vector: pWE18SFL3"
136..537
/notes="unnamed protein product"
/codon_start=1
/protein_id="BAC85873.1"
/db_xref="GI:34530325"
/translation="MVMLEDSSSGGARNVCVEFLVSLVGCQSRKQKQMTQOAG
PMLRAGRBASSSTNPGTLILDFOSPELPLAARQWQHEPVRGNLPHAFSSKCPGQ
YFPKSETQELNRVTVKRWELIISSENSGR"

CDS

Alignment Scores:
Pred. No.: 43e-51 Length: 4136
Score: 581.00 Matches: 114
Conservative: 1
Percent Similarity: 85.19%
Best Local Similarity: 84.44% Mismatches: 0
Query Match: 81.26% Indels: 20
DB: 9 Gaps: 1

US-10-005-907-2 (1-135) x AK124520 (1-4136)

QY 1 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys 20
DB 498 ATGGGAATATCTCTCGGAAACTC----- 524

QY 21 LysGlyAsnProLysGluGlyArgGlnGluMetThrThrPheGluArgLysLeu 40
DB 525 -----AGGAGGAATGACTCACTTTGAAGAACTT 557

QY 41 GlnPheArgGluLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGlu 60
DB 558 CAGCAACAGATAGAAAGCCAGAGTTTTCATCTCTTAATACGAAACGAGAAAT 617

QY 61 GlySerLysSerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer 80
DB 618 GGCAGTCTCTGGAAGAGTGCTACACTGTCTAATATCATCTCCCATCCAGAGATCC 677

QY 81 SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
DB 678 TCCCTGAGTCATGATGATGCTATGAGACATGCTCTCCCTCAGAGAAAGTGAGA 737

QY 101 GlnPheArgGluLysSerGlnGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro 120
DB 738 CAGTTTAGAAGAGTGAGAGACAGATATGCCCTTCTTAGAGCTTCTGTAGTAGGCTT 797

QY 121 CysSerCysThrHisGlnHisAspTyrGluValValPheProHis 135
DB 798 TGTCTCTGACCCATGAGCATGATTATGAGTTGTTGTTTCCACAC 842

RESULT 7
AC074365/c AC074365 141268 bp DNA linear HTG 23-SEP-2000
LOCUS Homo sapiens chromosome 1 clone RP11-11524, WORKING DRAFT SEQUENCE,
DEFINITION 10 unordered pieces.
ACCESSION AC074365
VERSION AC074365.5 GI:10280935
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 141268)
AUTHORS Waterston, R.H.

AY404586 Homo sapi
BQ214406 AGENCOURT
BG389415 602414106
AL560376 AL560376
BM904106 AGENCOURT
BM479887 AGENCOURT
BM455955 AGENCOURT
BG106563 602290373
BF795688 602295960
BM455198 AGENCOURT
CB286394 CND36 D01
AM983366 EST17E439
AM983366 AGENCOURT
AJ311038 EST181808
BG024891 602275814
BM459235 AGENCOURT
AY404587 Pan trogl
CE192340 tigr-gss-
CE020416 tigr-gss-
CD105480 AGENCOURT
BU746391 CH3#003 H
BU746392 CH3#003 H
BU96543 L22in1317
B19721 L22in1-Sp6 T
CE188479 tigr-gss-
CE091328 tigr-gss-
AG501175 V26GS mtn
BG145241 un88005.Y
BG145093 un88007.Y
BG276802 uv06d06.Y
BG276802 uv06d06.Y
CE207791 tigr-gss-
CE208849 AGENCOURT
AL222565 Tetraodon
AL062806 Drosophila
AL514529 AL514529
BU932945 AGENCOURT
BX367419 BX367419
CE790536 tigr-gss-
CE196221 tigr-gss-
BF264660 HV_CER001

5 58 14.3 508 29 AY404586
6 58 14.3 876 13 BQ214406
7 58 14.3 924 12 BG389415
8 58 14.3 987 9 AL560376
9 58 14.3 1000 12 BM904106
10 58 14.3 1039 12 BM479887
11 58 14.3 1070 12 BM455955
12 58 14.3 1095 12 BG106563
13 58 14.3 1124 10 BF795688
14 58 14.3 1193 12 BM455198
15 57.4 14.2 526 14 CB286394
16 56.4 13.9 683 10 AM983366
17 56.2 13.9 1165 12 AM983366
18 48.4 12.0 495 9 AJ311038
19 47.2 11.7 1041 10 BG024891
20 47 11.6 1059 12 BM459235
21 46.8 11.6 353 29 AY404587
22 46.6 11.5 259 29 CE192340
23 45.4 11.2 658 29 CE020416
24 45 11.1 967 14 CD105480
25 44.8 11.1 826 13 BU746391
26 44.8 11.1 840 13 BU746392
27 44.6 11.0 560 13 BU96543
28 44.6 11.0 774 28 B19721
29 44.4 11.0 731 29 CE188479
30 44 10.9 203 29 CE091328
31 44 10.9 421 28 AG501175
32 44 10.9 520 12 BG145241
33 44 10.9 522 12 BG145093
34 44 10.9 524 12 BG276802
35 44 10.9 526 12 BG276802
36 44 10.9 668 29 CE207791
37 44 10.9 825 14 CB320849
38 43.8 10.8 899 29 CNS03004
39 43.8 10.8 959 29 CNS00655
40 43.6 10.8 1201 9 AL514529
41 43.6 10.8 615 13 BU932945
42 43.4 10.7 404 13 BX367419
43 42.8 10.6 703 29 CE790536
44 42.8 10.6 756 29 CE196221
45 42.6 10.5 891 10 BF264660

ALIGNMENTS

RESULT 1
BF242113 527 bp mRNA linear EST 14-NOV-2000
LOCUS 601880401P1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109064 5',
DEFINITION mRNA sequence.
ACCESSION BF242113.1 GI:11156040
VERSION BF242113.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 527)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM993 row: a column: 01
High quality sequence stop: 518.

GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 13:36:26 ; Search time 2525 Seconds
(without alignments)
4789.775 Million cell updates/sec

Title: US-10-005-907-1_COPY_25_429

Perfect score: 405
Sequence: 1 atgggaataactctcg.....atgaagtgtgtttccacac 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estum:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_fod:*

26: em_gss_obg:*

27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	527	10	BF242113 601880401
2	64.8	16.0	288	10	AW480906 33516 MAR
3	59.6	14.7	1045	10	BF797507 602257174
4	58.6	14.5	1085	12	BM455407 AGENCOURT

FEATURES
source

Location/Qualifiers
1. 527
/organism="Homo sapiens"
/db_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4109064"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 55"
/notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: Sfil (ggcccttcggcc); Site 2: Sfil (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCACATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 100.0%; Score 405; DB 10; Length 527;
Best Local Similarity 100.0%; Pred. No. 6.1e-86;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAATATCTCTCGAAACTCAGTTGCTGGGAGAGATCAAAAGAGCCCAAG 60
DB 45 ATGGGAATATCTCTCGAAACTCAGTTGCTGGGAGAGATCAAAAGAGCCCAAG 104
QY 61 AAGGAACCCGATGAGGAGAAACGCGAGGAAATGATCTTGAAGAAACTT 120
DB 105 AAGGAACCCGATGAGGAGAAACGCGAGGAAATGATCTTGAAGAAACTT 164
QY 121 CAAGATCAAGATAGAAAGCCAGAAATTCATCTTCAATCAGAAACGAGAT 180
DB 165 CAAGATCAAGATAGAAAGCCAGAAATTCATCTTCAATCAGAAACGAGAT 224
QY 181 GGCAGTGGTTCGAGAAAGTGTGTACATCTGTCTAATCAGATCCCATCAGAGATCC 240
DB 225 GGCAGTGGTTCGAGAAAGTGTGTACATCTGTCTAATCAGATCCCATCAGAGATCC 284
QY 241 TCCTGAGCTCAAGATGATGCTGTACATCTGTCTAATCAGATCCCATCAGAGATCC 300
DB 285 TCCTGAGCTCAAGATGATGCTGTACATCTGTCTAATCAGATCCCATCAGAGATCC 344
QY 301 CAGTTTAGAAGGTCAGAGACAGATATGCCCTTCTAGGACTTCTGTAGTAGGCCT 360
DB 345 CAGTTTAGAAGGTCAGAGACAGATATGCCCTTCTAGGACTTCTGTAGTAGGCCT 404
QY 361 TGTTCTCGACCCATGAGCATGATTAAGTTGTGTTCCACAC 405
DB 405 TGTTCTCGACCCATGAGCATGATTAAGTTGTGTTCCACAC 449

RESULT 2

AM480906
LOCUS 33516 MARC 2P1G Sus scrofa CDNA 5', mRNA sequence. EST 09-JUL-2000
DEFINITION
ACCESSION AM480906
VERSION
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM
REFERENCE
AUTHORS
TITLE
Pig gene discovery by normalized cDNA-library sequencing and EST cluster assembly

JOURNAL
MEDLINE
PUBMED
COMMENT

Mamm. Genome 13 (6), 475-478 (2002)
22213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 156, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.960904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 19 row: F column: 21
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source

Location/Qualifiers
1. 288
/organism="Sus scrofa"
/db_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2P1G"
/notes="Vector: PCMV SPORTS; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Query Match 16.0%; Score 64.8; DB 10; Length 288;
Best Local Similarity 75.8%; Pred. No. 4e-05;
Matches 94; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 285 CACAGGAAAGTGGAGACAGTTTAGAGAAAGTCAGAGACAGATATGCCCTTCTTAGGAC 344
DB 2 CACAGGAAAGTGGAGACAGTTTAGAGAAAGTCAGAGACAGATATGCCCTTCTTAGGAC 61
QY 345 TTCCTGTAGT---AGGCTGTGTCACCCAGTCAGATGATTAAGTTGTGTTCC 401
DB 62 GACTTACATCCCAAGTTTCTCTCTATACCCCTGAGATGATTAAGTTGTGTTCC 121
QY 402 ACAC 405
DB 122 TCAC 125

RESULT 3

BF797507
LOCUS 60225174F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4340323 5', mRNA sequence. EST 12-JAN-2001
DEFINITION
ACCESSION BF797507
VERSION BF797507.1 GI:12102561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgbp@remail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9852 row: d column: 20

FEATURES

Source

Location/Qualifiers

1. 527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4109064"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH108 (T1 phage-resistant)"
/clone_lib="NTH MGC 55"
/notes="Organ: Bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcattcgcc); Site 2: SfiI (ggcattcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 100.0%; Score 405; DB 10; Length 527;
Best Local Similarity 100.0%; Fred. No. 6.1e-86;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGAATATATCTCTGGGAAACTCAGTTGCTGGGAGAGATCAAAAGAGCCCAAG 50
DB 45 ATGGGAATATATCTCTGGGAAACTCAGTTGCTGGGAGAGATCAAAAGAGCCCAAG 104
QY 61 AAGGAAACCCAGATGAGGAAAGAAACCGGAGGAATGACTACATTTGAAAGAAACTT 120
DB 105 AAGGAAACCCAGATGAGGAAAGAAACCGGAGGAATGACTACATTTGAAAGAAACTT 164
QY 121 CAAGATCAAGATAGAAAGCCAGAGATTTTCATCCACTTCTAATCAGGAAACGAGAT 180
DB 165 CAAGATCAAGATAGAAAGCCAGAGATTTTCATCCACTTCTAATCAGGAAACGAGAT 224
QY 181 GCGAGTGTCTGAGAGATGCTGACATGCTGATTAATCAATCCCATCAGAGATCC 240
DB 225 GCGAGTGTCTGAGAGATGCTGACATGCTGATTAATCAATCCCATCAGAGATCC 284
QY 241 TCCTGAGCTCCAGATGATGCTGATGAGAACTGACTTCCTCAGAGAACTGAGA 300
DB 285 TCCTGAGCTCCAGATGATGCTGATGAGAACTGACTTCCTCAGAGAACTGAGA 344
QY 301 CAGTTTAGAAGAACTGAGACAGAAATATGCCCTTCTTAGGACTTCTTTAGTAGCCT 360
DB 345 CAGTTTAGAAGAACTGAGACAGAAATATGCCCTTCTTAGGACTTCTTTAGTAGCCT 404
QY 361 TGTTCCTGCCCATGAGCATGATTGAGAGTTGTGTTTCCAC 405
DB 405 TGTTCCTGCCCATGAGCATGATTGAGAGTTGTGTTTCCAC 449

RESULT 2

AW480906 288 bp mRNA linear Ref 09-JUL-2000
LOCUS 33516 MARC 2P-G Sus scrofa cDNA 5', mRNA sequence
DEFINITION AW480906
ACCESSION AW480906
VERSION AW480906.1 GI:7050949
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Fahrbrugg S.C., Smith T.P.L., Fekking B.A., Cho J., White J.,
Vallet J., Wistner, Rohrer G.A., Pertea G., Sultana R.,
Quackenbush J. and Keefe J.W.
TITLE Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly